

## SEQUENCE PROTOCOL

5 <110> Degussa-Hüls AG  
Forschungszentrum-Jülich GmbH

10 <120> New nucleotide sequences coding for the thrE gene and process  
for the enzymatic production of L-threonine with coryneform  
bacteria.

15 <130> 990079 BT

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30 <170> Patent Proprietor Publication 2.1

35 <210> 1  
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<212> DNA

40 <213> Corynebacterium glutamicum ATCC14752

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<222> (398)..(1864)  
<223> thrE-Gen

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(A list of gene sequences is given at Line 30, German page 23 to Line  
36, German page 31.)

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agccaaggga aaagaaagcc cctaagcccc gtgttattaa atggagactc tttggagacc 120

60 tcaagccaaa aaggggcatt ttcatttaaga aaataccctt ttgacacctgtt gttattgagc 180

65 tggagaagag acttgaactc tcaacctacg cattacaagt gcgttgcgtc gccaattgcg 240  
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70 gtacatcaca atggaattcg gggctagagt atctggtaaa ccgtgcataaa acgacctgtg 360  
attggactct ttttccttgc aaaatgtttt ccagcgg atg ttg agt ttt gcg acc 415

Met Leu Ser Phe Ala Thr

1 5

75 ctt cgt ggc cgc att tca aca gtt gac gct gca aaa gcc gca cct ccg 463  
Leu Arg Gly Arg Ile Ser Thr Val Asp Ala Ala Lys Ala Ala Pro Pro  
10 15 20

80 cca tcg cca cta gcc ccg att gat ctc act gac cat agt caa gtg gcc 511  
Pro Ser Pro Leu Ala Pro Ile Asp Leu Thr Asp His Ser Gln Val Ala  
25 30 35

85 ggt gtg atg aat ttg gct gcg aga att ggc gat att ttg ctt tct tca 559  
Gly Val Met Asn Leu Ala Ala Arg Ile Gly Asp Ile Leu Leu Ser Ser  
40 45 50

90 ggt acg tca aac agt gat acc aag gtg caa gtt cga gcg gtg acc tct 607  
Gly Thr Ser Asn Ser Asp Thr Lys Val Gln Val Arg Ala Val Thr Ser  
55 60 65 70

g	c	g	t	a	t	g	c	c	t	g	t	a	t	g	g	a	t	a	t	g	a	t	g	655
Ala	Tyr	Gly	Leu	Tyr	Tyr	Thr	His	Val	Asp	Ile	Thr	Leu	Asn	Thr	Ile									
				75					80					85										
5	a	c	c	t	t	a	a	c	a	t	c	g	g	a	g	a	a	c	c	g	a	c	703	
	Thr	Ile	Phe	Thr	Asn	Ile	Gly	Val	Glu	Arg	Lys	Met	Pro	Val	Asn	Val								
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10	t	t	c	a	t	g	g	c	a	a	c	t	t	c	c	a	a	c	t	c	t	751		
	Phe	His	Val	Val	Gly	Lys	Leu	Asp	Thr	Asn	Phe	Ser	Lys	Leu	Ser	Glu								
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15	g	t	t	g	a	c	g	t	t	g	a	c	t	t	c	c	g	c	c	t	g	799		
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	Val	Ala	Glu	Lys	Ile	Leu	Asp	Glu	Leu	Glu	Gln	Ser	Pro	Ala	Ser	Tyr								
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				170			175				180													
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	Leu	Pro	Thr	Phe	Phe	Gln	Asn	Val	Val	Gly	Gly	Phe	Ile	Ala	Thr	Leu								
				200			205				210													
45	c	c	t	g	t	c	a	t	t	g	a	t	t	t	t	t	g	c	t	g	1087			
	Pro	Ala	Ser	Ile	Ala	Tyr	Ser	Leu	Ala	Leu	Gln	Phe	Gly	Leu	Glu	Ile								
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50	a	a	c	c	c	t	t	t	t	g	a	a	c	t	c	t	t	t	g	c	g	1135		
	Lys	Pro	Ser	Gln	Ile	Ile	Ala	Ser	Gly	Ile	Val	Val	Leu	Leu	Ala	Gly								
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20 ggc atc aca cca atg ctt cca ggt cta gca att tac cgc gga atg tac 1615  
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25 gcc acc ttg aat gat caa aca ctc atg ggt ttc acc aac att gcg gtt 1663  
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30 gct tta gcc act gct tca tca ctt gcc gct ggc gtg gtt ttg ggt gag 1711  
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35 tgg att gcc cgc agg cta cgt cgt cca cca cgc ttc aac cca tac cgt 1759  
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40 gca ttt acc aag gcg aat gag ttc tcc ttc cag gag gaa gct gag cag 1807  
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50 aat aaa agg taaaaatcaa cctgcttagg cgtctttcgc ttaaatagcg 1904  
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 Val Val Leu Leu Ala Gly Leu Thr Leu Val Gln Ser Leu Gln Asp Gly  
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 10 Pro Asn Tyr Ser Ser Thr Phe Ala Arg Ile Ile Ala Gly Gly Val Thr  
 305 310 315 320  
 Ala Ala Ala Phe Ala Val Gly Cys Tyr Ala Glu Trp Ser Ser Val Ile  
 15 325 330 335  
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 340 345 350  
 20 Val Val Tyr Leu Gly Pro Val Ser Ala Ala Ala Ile Ala Ala Thr Ala  
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 Val Gly Phe Thr Gly Gly Leu Leu Ala Arg Arg Phe Leu Ile Pro Pro  
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 25 Leu Ile Val Ala Ile Ala Gly Ile Thr Pro Met Leu Pro Gly Leu Ala  
 385 390 395 400  
 Ile Tyr Arg Gly Met Tyr Ala Thr Leu Asn Asp Gln Thr Leu Met Gly  
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 30 Phe Thr Asn Ile Ala Val Ala Leu Ala Thr Ala Ser Ser Leu Ala Ala  
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 Gly Val Val Leu Gly Glu Trp Ile Ala Arg Arg Leu Arg Arg Pro Pro  
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 cggcactcca gcaccgcaga tgctgatgtat caacaactac gaatacgtat cttagcgtat 180  
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 Gly Leu Leu Ala Arg Arg Phe Leu Ile Pro Pro Leu Ile Val Ala Ile  
 375 380 385  
 35 gcc ggc atc aca cca atg ctt cca ggt cta gca att tac cgc gga atg 1494  
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 Tyr Ala Thr Leu Asn Asp Gln Thr Leu Met Gly Phe Thr Asn Ile Ala  
 410 415 420  
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 425 430 435  
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 Glu Trp Ile Ala Arg Arg Leu Arg Arg Pro Pro Arg Phe Asn Pro Tyr  
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 Arg Ala Phe Thr Lys Ala Asn Glu Phe Ser Phe Gln Glu Glu Ala Glu  
 455 460 465  
 55 cag aat cag cgc cgg cag aga aaa cgt cca aag act aat cag aga ttc 1734  
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 470 475 480 485  
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 Gly Asn Lys Arg  
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&lt;210&gt; 4

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&lt;213&gt; Corynebacterium glutamicum ATCC13032

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35 40 45

20

Asp Ile Leu Leu Ser Ser Gly Thr Ser Asn Ser Asp Thr Lys Val Gln  
50 55 60

25

Val Arg Ala Val Thr Ser Ala Tyr Gly Leu Tyr Tyr Thr His Val Asp  
65 70 75 80Ile Thr Leu Asn Thr Ile Thr Ile Phe Thr Asn Ile Gly Val Glu Arg  
85 90 95

30

Lys Met Pro Val Asn Val Phe His Val Val Gly Lys Leu Asp Thr Asn  
100 105 110Phe Ser Lys Leu Ser Glu Val Asp Arg Leu Ile Arg Ser Ile Gln Ala  
115 120 125

35

Gly Ala Thr Pro Pro Glu Val Ala Glu Lys Ile Leu Asp Glu Leu Glu  
130 135 140

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145 150 155 160Met Met Gly Gly Ala Val Ala Val Leu Leu Gly Gly Gly Trp Gln Val  
165 170 175

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Ser Leu Ile Ala Phe Ile Thr Ala Phe Thr Ile Ile Ala Thr Thr Ser  
180 185 190Phe Leu Gly Lys Lys Gly Leu Pro Thr Phe Phe Gln Asn Val Val Gly  
195 200 205

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Gly Phe Ile Ala Thr Leu Pro Ala Ser Ile Ala Tyr Ser Leu Ala Leu  
210 215 220

55

Gln Phe Gly Leu Glu Ile Lys Pro Ser Gln Ile Ile Ala Ser Gly Ile  
225 230 235 240Val Val Leu Leu Ala Gly Leu Thr Leu Val Gln Ser Leu Gln Asp Gly  
245 250 255

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Ile Thr Gly Ala Pro Val Thr Ala Ser Ala Arg Phe Phe Glu Thr Leu  
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Ser Glu Ile Leu His Val Met Leu Pro Ala Met Glu Ser Ala Ala Ala  
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Pro Asn Tyr Ser Ser Thr Phe Ala Arg Ile Ile Ala Gly Gly Val Thr  
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Ala Ala Ala Phe Ala Val Gly Cys Tyr Ala Glu Trp Ser Ser Val Ile  
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Val Val Tyr Leu Gly Pro Val Ser Ala Ala Ala Ile Ala Ala Thr Ala  
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15 Val Gly Phe Thr Gly Gly Leu Leu Ala Arg Arg Phe Leu Ile Pro Pro  
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Ile Tyr Arg Gly Met Tyr Ala Thr Leu Asn Asp Gln Thr Leu Met Gly  
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Gly Val Val Leu Gly Glu Trp Ile Ala Arg Arg Leu Arg Arg Pro Pro  
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30 Arg Phe Asn Pro Tyr Arg Ala Phe Thr Lys Ala Asn Glu Phe Ser Phe  
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Gln Glu Glu Ala Glu Gln Asn Gln Arg Arg Gln Arg Lys Arg Pro Lys  
 35 465 470 475 480

Thr Asn Gln Arg Phe Gly Asn Lys Arg  
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